

BLAST Basic Local Alignment Search Tool

•

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

gb|Af011751| (9599 letters)

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|2327070|gb|AF011751.1|AF011751

Description

Hepatitis C virus strain H77 pCV-H77C polyprotein gene, complete cds

Molecule type

nucleic acid

Query Length

9599

Subject ID

gi|5420376|emb|AJ238799.1|

Description

Hepatitis C virus type 1b complete genome, isolate Con1

Molecule type

nucleic acid

Subject Length

9605

Program

BLASTN 2.2.21+ [Citation](#)

Reference

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.33271	1.28

K	0.620991	0.46
H	1.12409	0.85

Results Statistics

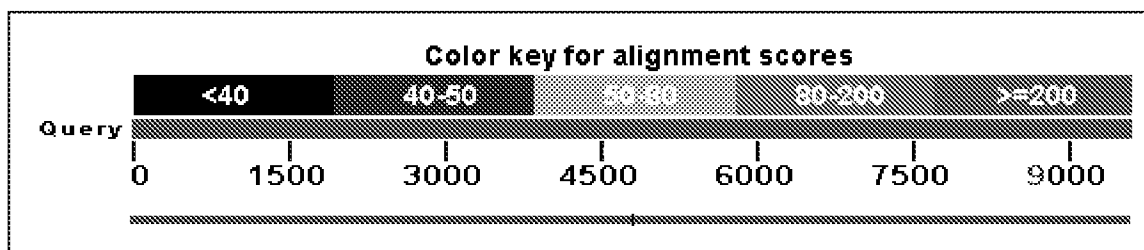
Effective search space 91853047


[Graphic Summary](#)

Distribution of 2 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[Dot Matrix View](#)


Plot of gi|2327070|gb|AF011751.1|AF011751 vs gi|5420376|emb|AJ238799.1 [\[?\]](#)

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



[Descriptions](#)

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

Accession	Subject	Length	Score	E-value	Identical
AJ238799.1	Hepatitis C virus type 1b complete genome, isolate 5956	9311	99%	0.0	79%
	Con1				

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>**emb|AJ238799.1|** Hepatitis C virus type 1b complete genome, isolate Con1
Length=9605

Sort alignments for this subject se
E value **Score** **Percent identity**
Query start position **Subject sta**

Score = 5956 bits (3225), Expect = 0.0
Identities = 7350/9298 (79%), Gaps = 458/9298 (4%)
Strand=Plus/Plus

Query	531	CCTATCCCCAAGGCACGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGG	590
Sbjct	531	CCTATCCCCAAGGCTCGCCAGCCCAGGGTAGGGCTGGGCTCAGCCCGGGTACCCTTGG	590
Query	591	CCCCTCTATGGCAATGAGGG-TTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTC	649
Sbjct	591	CCCCTCTATGGCAATGAGGGCTTG-GGGTGGGCGAGGATGGCTCCTGTACCCCCGTGGCTC	649
Query	650	TCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCAT	709
Sbjct	650	TCGGCCTAGTTGGGGCCCCACGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCAT	709
Query	710	CGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC	769
Sbjct	710	CGATACCCTCACGTGCGGCTTCGCCGATCTCATGGGGTACATTCCGCTCGTCGGCGCCCC	769
Query	770	TCTTGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA	829
Sbjct	770	CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA	829
Query	830	CTATGCAACAGGGAACCTTCTGGTTGCT-CTTTCTCTATCTTCCTTCTGGCCCTGCTCT	888
Sbjct	830	CTATGCAACAGGGAATCTGCCCGGTTGCTCCTTT-TCTATCTTCCTTTTGGCTTTGCTGT	888
Query	889	CTTGCCTGACTGTGCCC-GCTTCAGCCTACCAAGTGCGCAA--T-TCCTCGGGGCTTTAC	944
Sbjct	889	CCTGTTTGACCAT-CCCAGCTTCCGCTTATGAAGTGCGCAACGTAT-C-CGGAG-TGTAC	944
Query	945	CATGTCACCAATGATTGC-CCTAACTCGAGTATTGTGTACGAGGCGGCCG--ATGCCATC	1001
Sbjct	945	CATGTCACGAACGACTGCTCC-AACGCAAGCATTGTGTATGAGGCAGCGGACATG--ATC	1001
Query	1002	CTGCACACTCCGGGGTGTGT-CCCTTGCCTTCGCGAGGGTAACGCCTCGAGGTGTTGGGT	1060
Sbjct	1002	ATGCATACCCCCGGGTGCGTGCCC-TGCGTTTCGGGAGAACTCCTCCCGCTGCTGGGT	1060
Query	1061	GGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAAC-TCCCCACAACGCA-GCTTCGA	1118
Sbjct	1061	AGCGCTCACTCCCACGCTCGCGGCCAGGAAC-GCTAGCGTCCCCACTACG-ACGATACGA	1118
Query	1119	CGTCATATCGATCTGCTTGTCGGGAGC-GCCACCCTCTGCTCGGCCCTCTACGTGGGGGA	1177
Sbjct	1119	CGCCATGTCTGATTTGCTCGTTGGG-GCGGCTGCTCTCTGCTCCGCTATGTACGTGGGAGA	1177

Query	1178	CCTGTGCGGGTCTGTCTTT-CTTGTGGTCAACTGTTTACCTTCTCTCC-CAGGCGCCAC	1235
Sbjct	1178	TCTCTGCGGATCTGT-TTTCCTCGTCGCCCAGCTGTTACCTTCTCGCCTC-GCCGGCAC	1235
Query	1236	TGGACGAC-G--CAAGACTGCAATTGTTCTATCTATCCCGGCCATATAACGGGTTCATCGC	1292
Sbjct	1236	--GA-GACAGTACAGGACTGCAATTGCTCAATATATCCCGGCCACGTGACAGGTCAACGT	1292
Query	1293	ATGGCATGGGATATGATGATGAACTGGTCCCCTACGGCAGCGTTGGTGGTAGCTCAGCTG	1352
Sbjct	1293	ATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGGTATCGCAGTTA	1352
Query	1353	CTCCGGATCCCACAAGCCATCATGGACATGATCGTGGTGCTCACTGGGGAGTCCTGGCG	1411
Sbjct	1353	CTCCGGATCCCACAAGCTGTCTGGATATGGTGGCGGGGGCCCATGGGGAGTCCTAGCG	1412
Query	1413	GGCATAGCGTA-TTTCTCCATGGTGGGGAAGTGGGCGAAGGTCTGGTAGTGCTGCTGCT	1471
Sbjct	1413	GGCCTTGCCCTACTAT-TCCATGGTGGGGAAGTGGGCTAAGGTTCTGATTGTGATGCTACT	1471
Query	1472	ATTTGCCGGCGTCGACGCGGAAACCCACGTCACCGGGGAAATGCCGGCC-GCACCACGG	1530
Sbjct	1472	CTTTGCCGGCGTTGACGGGGGAACCTATGTGACAGGGGG-GACGATGGCCAAAACAC-C	1529
Query	1531	CT-GGGCTTGTTGGT--CTCCTTACACCAGGCGCCA-AGCAGAACATCCAAC-TGATCAA	1585
Sbjct	1530	CTCGGG-AT-TACGTCCCTCTTTTACCCGG-GTCATCCAGAAAATCCAGCTTG-TAAA	1585
Query	1586	CACCAACGGCAGTTGGCACATCAATAGCACGGCCTTGAATTGCAATGAAAGCCTTAACAC	1645
Sbjct	1586	CACCAACGGCAGCTGGCACATCAACAGGACTGCCCTGAACTGCAATGACTCCCTCAACAC	1645
Query	1646	-CGGCTGGTTAGCAGGGCTCTTCTATC-AACACAAATTCAACTCTTCAGGCTGTCTGAG	1703
Sbjct	1646	TGGGTTCCCTT-GCTGCGCTGTTCTA-CGTGCACAAGTTCAACTCATCTGGATGCCAGAG	1703
Query	1704	AGGTTGGCCAGCTGCCGACGCC-T-TACCGATTTTGCCAGGGCTGGGGTCTTATCAGTT	1761
Sbjct	1704	CGCATGGCCAGCTGCAG-CCCCATCGA-CGCGTTCGCTCAGGGGTGGGGGCCATCACTT	1761
Query	1762	ATGCCAACG-G--A-AGCGGCCTC-GACGA-ACGCCCTACTGCTGGCACTACCCTCCAA	1815
Sbjct	1762	A---CAATGAGTCACA-CAG-CTCGGACCAGA-GGCCTTATTGTTGGCACTACGCACCCC	1815
Query	1816	GACCTTGTGGCATTGTGCCCCGAAAG-AGCGTGTGTGGCCCGGTATATTGCTTCACTCCC	1874
Sbjct	1816	GGCCGTGCGGTATCGTACCCGCGGCGCAG-GTGTGTGGTCCAGTGACTGCTTAC-CCC	1873
Query	1875	-AGCCCCGTGGTGGTGGGAACGACCGACAGG-TCGGGCG-CGCCACCTACAGCTGGGGT	1931
Sbjct	1874	AAGCCCTGTCTGTTGGTGGGGACGACCGACCGGTTT-GGCGTC-CCTACGTACAGTTGGGG-	1930
Query	1932	GCA-AATGATACGGATGT-CTTCGTCCTTAACAACAC-CAGGCCACCGCTGGGCAATTGG	1988
Sbjct	1931	GGAGAATGAGACGGACGTGCTGC-TTCTTAACAACACGC-GGCCGCCGAAGGCAACTGG	1988
Query	1989	TTCGGTTGTACCTGGATGAACTCA--ACTGGATTACCAAAG-TGTGC-GGAGCGCCCCC	2044
Sbjct	1989	TTTGGCTGTACATGGATGAA-T-AGCACTGGGTTTACC-AAGACGTGCGGGGGC-CCCC	2044
Query	2045	TTGTGTCATCGGAGGGG-TGGGAACAACACCTTG-CTTGCCCCACTGATTGCTTCCGC	2102
Sbjct	2045	GTGTAACATCGG-GGGGATCGGCAATAAAACCTTGAC-CTGCCCCACGGACTGCTTCCGG	2102
Query	2103	AAACATCCGGAAGCCACATACTCTC-GGTGCGGCTCCGGTCCCTGGATT-ACACCCAGGT	2160
Sbjct	2103	AAGCACCCCGAGGCCACTTACAC-CAAGTGTGGTTTCGGGGCCTTGG-TTGACACCCAGAT	2160
Query	2161	GCATGGTCGACTACCCGTATAGGCTTTGGCACTATCCTTGTACCATCAA-TTACACCATA	2219
Sbjct	2161	GCTTGGTCCACTACCCATACAGGCTTTGGCACTACCCCTGCACTGTCAACTT-TACCATC	2219
Query	2220	TTCAAAGTCAGGATGTACGTGGGAGGG-GTCGAGCACAGGCTGGAAGCGGCCTGCAACTG	2278
Sbjct	2220	TTCAAGGTTAGGATGTACGTGGG-GGGAGTGGAGCACAGGCTCGAAGCCGCATGCAATTG	2278

Query	2279	GACGCGGGGCGAACGCTGTGATCTGGAAGACAGGGACAGGTCGAGCTCAGCCCGTTGCT	2338
Sbjct	2279	GACTCGAGGAGAGCGTTGTAACCTGGAGGACAGGGACAGATCAGAGCTTAGCCCGCTGCT	2338
Query	2339	GCTGTCCACCACACAGTGGCAGGTCCTT-CCGTGTTCTTTACGACCCTGCCAGCCT-TG	2396
Sbjct	2339	GCTGTCTACAACGGAGTGGCAGGT-ATTGCCCTGTTCTTACCACCCTACC-GGCTCTG	2396
Query	2397	TCCACCGGCCTCATCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGGTA	2456
Sbjct	2397	TCCACTGGTTTGTATCCATCTCCATCAGAACGTCGTGGACGTACAATACCTGTACGGTATA	2456
Query	2457	GGGTCAAAGC-ATCG-CGTCCTGGGCCATTAAAGTGGGAGTACGTCGT-TCTCCTGTTCTTT	2513
Sbjct	2457	GGGTC-GGCGGTTGTC-TCCTTTGCAATCAAATGGGAGTATGTCCTGT-TGCTCTTCTTT	2513
Query	2514	CTGCTTGACAGCGCGCGCTCTGCT-CCTGCTTGTGGATGATGTTACTCATATCCCAAGC	2572
Sbjct	2514	CTTCTGGCGGACGCGCGCGCTCTG-TGCCTGCTTGTGGATGATGCTGCTGATAGCTCAAGC	2572
Query	2573	GGAGGCGGCTTTGGAGAACCTCGTAATACTCAATGCAGCATCCCTGGCCGGGACGCACGG	2632
Sbjct	2573	TGAGGCCGCCCTAGAGAACCTGGTGGTCTCAACGCGGCATCCGTGGCCGGGGCGCATGG	2632
Query	2633	TC-TTGTTGTCCTTCTCTCGTGTCTTCTGCT-TTGCCTGGTATC-TGAAGGGTAGG-TGGG	2688
Sbjct	2633	-CATTCTCTCCTTCTCTCGTGTCTTCTG-TGCTGCCTGGTA-CATCAAGGGCAGGCT-GG	2688
Query	2689	TGCCC-GGAGCGGTC-TACGCCCTCTACGG-GATGTGGCCTCTCTCTGCTCCTGCTGG	2745
Sbjct	2689	T-CCCTGGGGCGG-CATATGCCCTCTACGGCG-TATGGCCGCTACTCCTGCTCCTGCTGG	2745
Query	2746	CGTTGCC-TCAGCGGGCATAACG-CACTGGACAC-GGAGGTGGCCGCGTCGTGTGGCGGCG	2802
Sbjct	2746	CGTTACCACCA-CGAGCATAACCCA-TGGAC-CGGGAGATGGCAGCATCGTGCAGGAGGCG	2802
Query	2803	TTGTTCTT-GTCGGGT-TAATGGCGC-TGA-CTCTGTCGCCATATTACAAGC-GCTAT-A	2856
Sbjct	2803	CGGTT-TTCGT-AGGTCTGAT-ACTCTTGACCT-TGTCACCGCACTATAAGCTG-T-TCC	2856
Query	2857	TCAGCT-GG-TGCATGTGGTGGCTT-CAGTATTTTCTGACCAGAGTAGAAGCGCA-AC-T	2911
Sbjct	2857	TC-GCTAGGCT-CATATGGTGG-TTACAATATTTATCACCAGGGCCG-AG-GCACACTT	2911
Query	2912	GCACGTGTGGGTTccccccTCAACGTCCggggggCGCGATGCCGTCATCTTACTCAT	2971
Sbjct	2912	GCAAGTGTGGATCCCCCCCCTCAACGTTCCGGGGGGCCGCGATGCCGTCATCCTCCTCAC	2971
Query	2972	GTGTGTAG-TACACCC-GACCCTGGTATTTGA-CATCACCAAACCTAC-TCCTGGCCAT-C	3026
Sbjct	2972	GTGCG-CGATCCACCCAGA-GCTAATCTTT-ACCATACCAAAAT-CTTGCTCGCCATAC	3027
Query	3027	TTCGGACCCCT-TTGGATTCTTCAAGCCAGT-TTGCTTAAAGTCCCTACTTCGTGCGCG	3084
Sbjct	3028	-TCGGTCCACTCATGG-TGCTCCAGGCTGGTATAAC-CAAAGTGCCGTACTTCGTGCGCG	3084
Query	3085	TTCAAGGCCTTC-TCCGGAT-C-TGCGCGCTAGCGCGGAAGATAGCCGGAGGTCATTACG	3141
Sbjct	3085	CACACGGGC-TCATTC-G-TGCATGCATGCTGGTGCAGGAGGTTGCTGGGGGTCATTATG	3141
Query	3142	TGCAAATGGC-CATCATCAAGTTAGG-GGCGCTTACTGGCACCTATGTGTATAACCATCT	3199
Sbjct	3142	TCCAAATGGCTC-TCATGAAGTT-GGCCGCACTGACAGGTACGTACGTTTATGACCATCT	3199
Query	3200	CACCCCTCTTCGAGACTGGGCGCACAAAC-GGCCTGCGAGATCTGGCCGTGGCTGTGGAAC	3258
Sbjct	3200	CACCCCACTGCGGGACTGGGCCAC-GCGGGCCTACGAGACCTTGCCTGGCAGTTGAGC	3258
Query	3259	CAGTCGTCTTCTCCCGA-ATGGAGACCAAGCTCATCACGTGGGGGGCAGATACCGCCGCG	3317
Sbjct	3259	CCGTCTCTTCT-CTGATATGGAGACCAAGGTTATCACCTGGGGGGCAGACACCGCGGCG	3317
Query	3318	TGCGGTGACATCATCAACGGCTTGCCCGTCTCTGCCCGTAGGGGCCA-GGAGATAC-TGC	3375
Sbjct	3318	TGTGGGGACATCATCTTGGGCCTGCCCGTCTCCGCCCGCAGGGG-GAGGGAGATACAT-C	3375

```
Query 3376 TTGGG-CCAGCCGAC-GGAATGGTCTCCAAGGGGTGGAGGTTGCTGGCGCCCATCACGGC 3433
Sbjct 3376 -TGGGACCGGCAGACAGCCTTGAAGGGC-AGGGGTGGCGACTCCTCGCGCCTATTACGGC 3433
Query 3434 GTACGCCCAGCAGACGAGAGGCCTCCTAGGGTGTATAATCACCAGCCTGACTGGCCGGGA 3493
Sbjct 3434 CTACTCCCAACAGACGCGAGGCCTACTTGGCTGCATCATCACTAGCCTCACAGGCCGGGA 3493
Query 3494 CAAAAACCAAGTGGAGGGTGAAGTCC-AGATCGTGTCAACTGCTACCCAAACCTTCCTGG 3552
Sbjct 3494 CAGGAACCAGGTCGAGGGGGAGGTCCAAG-TGGTCTCCACCGCAACACAATCTTTCCTGG 3552
Query 3553 CAACGTGCATCAATGGGGTATGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCG 3612
Sbjct 3553 CGACCTGCGTCAATGGCGTGTGTGGACTGTCTATCATGGTGCCGGCTCAAAGACCCTTG 3612
Query 3613 -CATCACCCAAGGGTCCTGTCTATCCAGATGTATACCAATGTGGACCAAGACCTTGTGGGC 3671
Sbjct 3613 CCGGC-CCAAAGGGCCCAATCACCCAAATGTACACCAATGTGGACCAGGACCTCGTCGGC 3671
Query 3672 TGGCCCGCTCCTCAAGGTTCCCGCTCATTGACACCCTGTACCTGCGGCTCCTCGGACCTT 3731
Sbjct 3672 TGGCAAGCGCCCCCGGGGCGCGTTCCTTGACACCATGCACCTGCGGCAGCTCGGACCTT 3731
Query 3732 TACCTGGTCACGAGGCACGCCGATGTCAATCCCGTGCGCCGGCGAGGTGATAGCAGGGGT 3791
Sbjct 3732 TACTTGGTCACGAGGCATGCCGATGTCAATCCCGTGCGCCGGCGGGGCGACAGCAGGGGG 3791
Query 3792 AGCCTGCTTTTCGCCCC-GGCCATTTCCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTT 3850
Sbjct 3792 AGCCTACTCTC-CCCCAGGCCCGTCTCCTACTTGAAAGGCTCTTCGGGCGGTCCACTGCT 3850
Query 3851 GTGCCCCGCGGGACACGCCGTGGGC--CTATTAGGGCCGCGGTGTGCACCCGTGGAGTG 3908
Sbjct 3851 CTGCCCCCTCGGGGACGCTGTGGGCATCT-TTC-GGGCTGCCGTGTGCACCCGAGGGGTT 3908
Query 3909 GCTAAAGCGGTGGACTTTTAT-CCCTGTGGAGAACCTA-GG-GACAACCATGAGATCCCCG 3965
Sbjct 3909 GCGAAGGCGGTGGACTTTGTACCC-GTCGAG--TCTATGGAAACCACTATGCGGTCCCCG 3965
Query 3966 GTGTTACGGACAACCTCCTCTCCACCAGCAGTGCCCCAGAGC-TTCCAGGTGGCCACCT 4024
Sbjct 3966 GTCTTACGGACAACCTCGTCCCTCCGGCCGTACCGCAGA-CATTCCAGGTGGCCCATCT 4024
Query 4025 GCATGCTCCC-ACCGGCAGCGGTAAGAGCACCAAGGTCCCGGCTGCGTACGCAGCCC-AG 4082
Sbjct 4025 ACACGC-CCCTACTGGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCGTATGCAGCCCAAG 4083
Query 4083 GGCTACAAGGTG-TTGGTGCTCAACCCCTCTGTTGCTGCAACGCTGGGCTTT-GGTGCTT 4140
Sbjct 4084 GG-TATAAGGTGCTT-GTCCTGAACCCGTCCGTGCCGCCACCCTAGG-TTTCGGGGCGT 4140
Query 4141 ACATGTCCAAGGCCCATGGGGTTGATCCTAATATCAGGACCGGGGTGAGAACAATTACCA 4200
Sbjct 4141 ATATGTCTAAGGCACATGGTATCGACCCTAACATCAGAACCAGGGTAAGGACCATACCA 4200
Query 4201 CTGGCAG-CCCCATCACGTACTCCACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCA 4259
Sbjct 4201 C-GGGTGCCCCCATCACGTACTCCACCTATGGCAAGTTTCTTGCCGACGGTGTTGCTCT 4259
Query 4260 GGAGGTGCTTATGACATAATAATTTGTGACGAGTGCCACTCCACGGA-TGCCA-CATCCA 4317
Sbjct 4260 GGGGGCGCCTATGACATCATAATATGTGATGAGTGCCACTCAACTGACT-CGACCA-CTA 4317
Query 4318 TCTTGGGCATCGGCACTGTCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGC 4377
Sbjct 4318 TCCTGGGCATCGGCACAGTCTTGACCAAGCGGAGACGGCTGGAGCGCGACTCGTCGTGC 4377
Query 4378 TCGCCACTGCTACCCCTCCGGGCTCCGTCACTGTGTCC-CATCCTAACATCGAGGAGGTT 4436
Sbjct 4378 TCGCCACCGCTACGCCTCCGGGATCGGTCAACGTG-CCACATCAAACATCGAGGAGGTG 4436
Query 4437 GCTCTGTCCACCACCGAGAGATCCCCTTTTACGGCAAGGCTATCCCCCTCGAGGTGATC 4496
Sbjct 4437 GCTCTGTCCAGCACTGGAGAAATCCCCTTTTATGGCAAAGCCATCCCCATCGAGACCATC 4496
```

Query	4497	AAGGGGGGAAGACATCTCATCTTCTGCCACTCAAAGAAGAAGTGCACGAGCTCGCCGCG	4556
Sbjct	4497	AAGGGGGGGGAGGCACCTCATTCTTCTGCCATTCCAAGAAGAAATGTGATGAGCTCGCCGCG	4556
Query	4557	AAGCTGGT-C-GCATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCTG	4614
Sbjct	4557	AAGCT-GTCCGGCCTCGGAC-TCAATGCTGTAGCATATTACCGGGGCCCTTGATGTATCCG	4614
Query	4615	TCATCCCGACCAGCGGCGATGTTGTCTCGT-GTCGACCGATGCTCTCATGACTGGCTTT	4673
Sbjct	4615	TCATACCAACTAGCGGAGACGTCATTGTCTGTAG-CAACGGACGCTCTAATGACGGGCTTT	4673
Query	4674	ACCGGCGACTTCGACTCTGTGATAGACTGCAACACGTGTGTCACTCAGACAGTCGATTTT	4733
Sbjct	4674	ACCGGCGATTTTCGACTCAGTGATCGACTGCAATACATGTGTCAACCAGACAGTCGACTTC	4733
Query	4734	AGCCTTGACCCTACCTTTACCATTGAGACAACCA-CGCTCCCCCAGGATGCTGTCTCCA-	4791
Sbjct	4734	AGCCTGGACCCGACCTTCACCATTGAGACGACGACCG-TGCCACAAGACGCGGTGT-CAC	4791
Query	4792	GGACTCAACGCCGGGGCAGGACTGGCAGGGGGAAGCCAGGCATCTATAGATTTGTGGCAC	4851
Sbjct	4792	GCTCGCAGCGGCGAGGCAGGACTGGTAGGGGCAGGATGGGCATTTACAGGTTTGTGACTC	4851
Query	4852	CGGGGGAGCGCCCTCCGGCATGTTTCGACTCGTCCGTCCTCTGTGAGTGCTATGACGCGG	4911
Sbjct	4852	CAGGAGAACGGCCCTCGGGCATGTTTCGATTCTCGGTTCTGTGCGAGTGCTATGACGCGG	4911
Query	4912	GCTGTGCTTGGTATGAGCTCACGCCCGCCGAGAC-TACAGTTAGGCTACGAGCGTACATG	4970
Sbjct	4912	GCTGTGCTTGGTACGAGCTCACGCCCGCCGAGACCT-CAGTTAGGTTGCGGGCTTACCTA	4970
Query	4971	AACACCCCGGGGCTT-CCCGTGTGCCAGGACCATCTTGAATTTTGGGAGGGCGTCTTTAC	5029
Sbjct	4971	AACACACCAGGG-TTGCCCGTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTAC	5029
Query	5030	GGGCCTCACTCATATAGATGCCCACTT-TTATCCCAGACAAAGCAGAGTGGG-GAGAAC	5087
Sbjct	5030	AGGCCTCACCCACATAGACGCCCA-TTCTTGTGCCAGACTAAGCAG-GCAGGAGACAAC	5087
Query	5088	TTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCCA	5147
Sbjct	5088	TTCCCCTACCTGGTAGCATACCAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCA	5147
Query	5148	TCGTGGGACCAGATGTGGAAGTGTTTGATCCGCCTTAAACCC-ACCCTCCATGGGCCAAC	5206
Sbjct	5148	TCGTGGGACCAAATGTGGAAGTGCTCATAACGGCT-AAAGCCTACGCTGCACGGGCCAAC	5206
Query	5207	ACCCCTGCTATACAGACTGGGCGCTGTTTCAAGTGAAGTCAC--CCTGACGCACCCAATC	5264
Sbjct	5207	GCCCCTGCTGTATAGGCTGGGAGCCGTTCAAACAGAGGTTACTACC--ACACACCCCATATA	5264
Query	5265	ACCAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTCGTACGAGCACCTGGGTG	5324
Sbjct	5265	ACCAAATACATCATGGCATGCATGTCGGCTGACCTGGAGGTCGTACGAGCACCTGGGTG	5324
Query	5325	CTCGTTGGCGGCGTCTGGCTGCTCTGGCCGCGTATTGCCTGTCAACAGGCTGCGTGGTC	5384
Sbjct	5325	CTGGTAGGCGGAGTCTTAGCAGCTCTGGCCGCGTATTGCCTGACAACAGGCAGCGTGGTC	5384
Query	5385	ATAGTGGGCAGGATCGTCTTGTCCGGGAAGCCGGCAATTATACCTGACAGGGAGGTTCTC	5444
Sbjct	5385	ATTGTGGGCAGGATCATCTTGTCCGGAAAGCCGGCCATCATTCCCGACAGGGAAGTCCTT	5444
Query	5445	TACCAGGAGTTTCGATGAGATGGAAGAGTGCTC-TCAGCACTTACCGTACATCGAGCAAGG	5503
Sbjct	5445	TACCGGGAGTTTCGATGAGATGGAAGAGTGCGCCTCA-CACCTCCCTTACATCGAACA-GG	5502
Query	5504	GA-TG-ATGCTCGCTGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCC	5561
Sbjct	5503	GAATGCA-GCTCGCCGAACAATTCAAACAGAAGGCAATCGGGTTGCTGCAAACAGCCACC	5561
Query	5562	C-GCCATGCAGAGGTTA-T-CACCCCTGCTGTCCAGACCAACTGGCAGAACTCGAGGTC	5618
Sbjct	5562	AAGCAA-GCGGAGGCTGCTGCTCCCGTGGTGGA-AT-CCAAGTGGCGGACCCTCGAAGCC	5618


```
Query 5619 TTTTGGGCGAAGCACATGTGGAATTTTCATCAGTGGGATACAATACTTGGCGGGCCTGTCA 5678
      |||
Sbjct 5619 TTCTGGGCGAAGCATATGTGGAATTTTCATCAGCGGGATACAATATTTAGCAGGCTTGTCC 5678

Query 5679 ACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGC-TGCCGTACCAG 5737
      |||
Sbjct 5679 ACTCTGCCTGGCAACCCCGCGATAGCATCACTGATGGCATTACAGCCT-CTATCACCAG 5737

Query 5738 CCCACTAACCCTGGCCAAACCCCTCCTCTTCAACATATTggggggTGGGTGGCTGCCCA 5797
      |||
Sbjct 5738 CCCGCTCACCACCCAACATACCCTCCTGTTTAAACATCCTGGGGGGATGGGTGGCCGCCCA 5797

Query 5798 GCTCGCCGCC-CCCGGTGCCGCTACTGCCTTT-GTGGGTGCTGGCCTAGCTGGCGCCGCC 5855
      |||
Sbjct 5798 ACTTGCT-CCTCCCAGCGCTGCTTCTGC-TTTCGTAGGCGCCGGCATCGCTGGAGCGGCT 5855

Query 5856 ATCGGCAGCGTTGGACTGGGGAAGGTCTCTGTTGACATTCTTG-CAGGGTATGGCGC-GG 5913
      |||
Sbjct 5856 GTTGGCAGCATAGGCCCTTGGGAAGGTGCTTGTGGATATT-TTGGCAGGTTATGGAGCAGG 5914

Query 5914 GCGTGGCGGGAGCTCTTGTAGCATTCAAGATCATGAGCGGTGAGGTCCCCTCCACGGAGG 5973
      |||
Sbjct 5915 G-GTGGCAGGCGCGCTCGTGGCCTTTAAGGTCATGAGCGGCGAGATGCCCTCCACCAGG 5973

Query 5974 ACCTGGTCAATCTGCTGCCC-GCCATCCTCTCGCCTGGAGCCCTTGTAGTCGGTGTGGTC 6032
      |||
Sbjct 5974 ACCTGGTTAACTACT-CCCTGCTATCCTCTCCCCTGGCGCCCTAGTCGTCGGGGTCTGTG 6032

Query 6033 TGCGCAGCAATACTGCGCCGGCACGTTGGCCC-GGGCGAGGGGGCAGTGCAATGGATGAA 6091
      |||
Sbjct 6033 TGCGCAGCGATACTGCGTCGGCACGTGGGCCCAGGG-GAGGGGGCTGTGCAGTGGATGAA 6091

Query 6092 CCGGCTAATAGCCTTCGCCTCCCGGGGAACCATGTTTCCCCACGCACACTACGTGCCGGA 6151
      |||
Sbjct 6092 CCGGCTGATAGCGTTTCGCTTCGCGGGGTAACCACGTCTCCCCACGCACACTATGTGCCTGA 6151

Query 6152 GAGCGATGCAGCCGCCCGCGTCACTGCC-ATACTCAGC-AGCCTCACTGTAACCCAGCTC 6209
      |||
Sbjct 6152 GAGCGACGCTGCAGCACGTGTCACT-CAGATCCTCT-CTAGTCTTACCATCACTCAGCTG 6209

Query 6210 CTGAGGCGACTGCATCAGTGGAT-AAGCTCGGAGTG-TACCCTCATGCTCCGGTTTCCT 6267
      |||
Sbjct 6210 CTGAAGAGGCTTCACCACTGGATCAA-CGAGGACTGCT-CCACGCCATGCTCCGGCTCGT 6267

Query 6268 GGCTAAGGGACATCTGGGACTGGATATGCGA-GGTGCTGAGC-GACTTT-AAGACCTGGC 6324
      |||
Sbjct 6268 GGCTAAGAGATGTTTGGGATTGGATATGC-ACGGTGTGTA-CTGA-TTTCAAGACCTGGC 6324

Query 6325 TGAAAG-CCAAGCTCATGCCACAACCTGCCTGGGATTCCCTTTGTGTC-C-TGCCAGCGCG 6381
      |||
Sbjct 6325 TCCA-GTCCAAGCTCCTGCCGCGATTGCC-GGGAGTCCCTTCT-TCTCATGTCAACGTG 6381

Query 6382 GGTATAGGGGGTCTGGCGAGGAGACGGCATTATGCACACTCGC-TGCC-ACTGTGGAGC 6439
      |||
Sbjct 6382 GGTACAAGGGAGTCTGGCGGGGCGACGGCATCATGCAAAC-CACCTGCCCA-TGTGGAGC 6439

Query 6440 TGAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCCTAGGACCTGCAG 6499
      |||
Sbjct 6440 ACAGATCACCAGGACATGTGAAAAACGGTTCCATGAGGATCGTGGGGCCTAGGACCTGTAG 6499

Query 6500 GAACATGTGG-AGTGGGACGTTCCCCATTAACGCCTACACCACGGGCCCCCTGTACTCCCC 6558
      |||
Sbjct 6500 TAACACGTGGCA-TGGAACATTCCCCATTAACGCGTACACCACGGGCCCCCTGCACGCCC- 6557

Query 6559 TTCCTG-CGCCGAACATAAGTTCG-CGCTGTGGAGGGTGTCTGCAGAGGAATACGTGGA 6616
      |||
Sbjct 6558 TCCCCGGCGCCAAATTATTC-TAGGGCGCTGTGGCGGGTGGCTGCTGAGGAGTACGTGGA 6616

Query 6617 GATAAGGCGGGTGGGGGACTTCCACTACGT-ATCGGGTATGACTACTGACAATCTTAAA- 6674
      |||
Sbjct 6617 GGTTACGCGGGTGGGGGATTTCCACTACGTGA-CGGGCATGACCACTGACAA-CGTAAAG 6674

Query 6675 TGCCCGTGCCAGATCCCATCGCCCGAATTTTTACAGAATTGGACGGGGTGCGCCTACAC 6734
      |||
Sbjct 6675 TGCCCGTGTCAAGTTCCGGCCCCCGAATTCTTACAGAAGTGGATGGGGTGCGGTTGCAC 6734
```

Query	6735	AGGTTTTCGCCCCCTTGCAAGCCCTTGCTGCGGGAGGAGGT-ATCATTCA-GAGTAGGAC	6792
Sbjct	6735	AGGTACGCTCCAGCGTCAAACCCCTCCTACGGGAGGAGGTCA-CATTCTTG-GTCGGGC	6792
Query	6793	TCCA-CGAGTACCCGGTGGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTAGCCGTG	6851
Sbjct	6793	TCAATCAA-TACCTGGTTGGGTACAGCTCCCATGCGAGCCCGAACCGGACGTAGCAGTG	6851
Query	6852	TTGACGTCCATGCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGAGAAGGTTG	6911
Sbjct	6852	CTCACTTCCATGCTCACCAGCCCCCTCCACATTACGGCGGAGACGGCTAAGCGTAGGCTG	6911
Query	6912	GCGAGAGGG-TCACCCCCTTC-TATGGCCAGCTCCTCGGCTAGCCAGCTGTCCGCTCCAT	6969
Sbjct	6912	GCCAG-GGGATCTCCCCCTCCT-TGGCCAGCTCATCAGCTAGCCAGCTGTCTGCGCCTT	6969
Query	6970	CTCTC-AAGGCAACTTGACCCGCCAACCATGACTCCCCTGACGCCGAGCTCATAGAGGCT	7028
Sbjct	6970	C-CTTGAAGGCAACATGCACTACCCGTCACTGACTCCCCGGACGCTGACCTCATCGAGGCC	7028
Query	7029	AACCTCCTGTGGAGGCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAGAACAAA	7088
Sbjct	7029	AACCTCCTGTGGCGGCAGGAGATGGGCGGGAACATCACCCGCGTGGAGTCAGAAAATAAG	7088
Query	7089	GTGGTGATTCTGGACTCCTTCGATCCGCTTGTTGGCAGAGGAGGATGAGCGGGAGGTCTCC	7148
Sbjct	7089	GTAGTAATTTTGGACTCTTTCGAGCCGCTCCAAGCGGAGGAGGATGAGAGGGAAGTATCC	7148
Query	7149	GTACCTGCAGAAATTCTGCGGAAGTCTC-GGAGATTGCC-CGGGCCCTGCCCGTCTGGG	7206
Sbjct	7149	GTTCCGGCGGAGATCCTGCGGAGGTC-CAGGAAATTC-CCTCGAGCGATGCCCATATGGG	7206
Query	7207	CGCGGCCGGACTACAACCCCCGCTAGT-AGAGACGTGGAAAAAGCCTGACTACGAACCA	7265
Sbjct	7207	CACGCCCGGATTACAACCTTCCACT-GTTAGAGTCCTGGAAGGACCCGGACTACGTCCCT	7265
Query	7266	CCTGTGGTCCATGGCTGCCCCGTACCACCT-CCACGGTCCCCCTCTG-TGCCTCCGCCTC	7323
Sbjct	7266	CCAGTGGTACACGGGTGTCCATTGCCGCCTGCCAAGG-CCCCTCC-GATACCACCTCCAC	7323
Query	7324	GGAAAAAGCGTACGGTGGTCTCTACCGAATCAACCCTATCTACTGCCTTGGCCGAGCTTG	7383
Sbjct	7324	GGAGGAAGAGGACGGTTGTCTGTGAGAATCTACCGTGTCTTCTGCCTTGCGGAGCTCG	7383
Query	7384	CCACCAAA-AGTTTTGGCAGCTCCTCAA-CTTCCGGCATT--ACGGGCACAATACGACA	7439
Sbjct	7384	CCAC-AAAGACCTTCGGCAGCTCCG-AATCGTC-GGCCGTCGACAG-CGGCA---CGGCA	7436
Query	7440	ACATCCTCTGA-GCCC-GCCCCTTCTG--G-CTG-----G-ACTCCGACGTTGAGTCC	7493
Sbjct	7437	ACGGCCTCTCTTGACCAGCCC-TCC-GACGACGGCGACGCGGGA-TCCGACGTTGAGTCG	7493
Query	7494	TATTCTTCCATG-----TGGAGGGGGAGCCTGGGGATCCGGATCTCAGCGACGGGTCA	7553
Sbjct	7494	TACTCCTCCATGCCCCCCTTGAGGGGGAGCCGGGGGATCCCGATCTCAGCGACGGGTCT	7553
Query	7554	TGGTCGACGGTCAGTAGTGG-GGCCGACACGGAAGATGTCGTGTGCTGCTCAATGTCTTA	7612
Sbjct	7554	TGGTCTACCGTAAGC-GAGGAGGCT-AGT-G-AGGACGTCTGTGCTGCTCGATGTCCTA	7609
Query	7613	TTCTTGACAGGCGCACTCG-TCACCCCGTGCCTGCGGAAGAA-CAAAAAC TGCCATC	7670
Sbjct	7610	CACATGGACAGGCGCCCT-GATCACGCCATGCGCTGCGGAGGAAACCAAG-CTGCCCATC	7667
Query	7671	AACGCACTGAGCAACTCGTTGCTACGCCATCACAATCT-GGTGTATTCCACCACTTCACG	7729
Sbjct	7668	AATGCACTGAGCAACTCTTTGCTCCGTCACCACAA-CTTGGTCTATGCTACAACATCTCG	7726
Query	7730	CAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGACAGACTGCAAGTTCTGGAC-AGCC	7788
Sbjct	7727	CAGCGCAAGCCTGCGGCAGAAGAAGGTCACCTTTGACAGACTGCAGGTCTTGACGA-CC	7785
Query	7789	ATTACCAGGACGTGCTCAAGGAGGTCAAAGC-AGCGGCGTCAAAAGTGAAGGCTAA-CTT	7846
Sbjct	7786	ACTACCGGGACGTGCTCAAGGAGATGAAGGCGAA-GGCGTCCACAGTTAAGGCTAAACTT	7844

Query	7847	GCTATCCGTAGAGGAAGCTTGCA-GCCTGACGCCCCACATTCAGCCAAATCCAAGTTTG	7905
Sbjct	7845	-CTATCCGTGGAGGAAGCCTGTAAGC-TGACGCCCCACATTCGCCAGATCTAAATTTG	7902
Query	7906	GCTATGGGGCAAAGACGTCCGTTGCC-ATGCCAGAAAGGCCGT-AGCCCACATCAACTC	7963
Sbjct	7903	GCTATGGGGCAAAGGACGTCCGGAACCTAT-CCAGCAAGGCCGTTAACC-ACATCCGCTC	7960
Query	7964	CGTGTGGAAAGACCTT-CTGGAAGACAGTGTA-ACACCAATAGACACTACCATCATGGCC	8021
Sbjct	7961	CGTGTGGAAAGGAC-TTGCTGGAAGACACTG-AGACACCAATTGACACCACCATCATGGCA	8018
Query	8022	AAGAACGAGGTTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAGCCAGCTCGTCTCATC	808
Sbjct	8019	AAAAATGAGGTTTTTCTGCGTCCAACCAGAGAAGGGGGGCCGAAGCCAGCTCGCCTTATC	8078
Query	8082	GTGTTCCCCGACCTGGGCGTGCGGTGTGCGAGAAGATGGCCCTGTACGACGTGGT-TAG	8140
Sbjct	8079	GTATTCCCAGATTTGGGGGTTCGTGTGTGCGAGAAATGGCCCTTTACGATGTGGTCTC-	8137
Query	8141	CAAGCTCCCCCTGGCCGTGATGGGAAGCTCC-TACGGATTCCAATACTCACCAGGACAGC	8199
Sbjct	8138	CACCCCTCCCTCAGGCCGTGATGGGCT-CTTCATACGGATTCCAATACTCTCCTGGACAGC	8196
Query	8200	GGGTTGAATTCTCTGTGCAA-GCGTGGAA-GTCCAAGAAGAC-CCCgatggggTTCTCGT	8256
Sbjct	8197	GGGTCGAGTTCTCTGGTG-AATGCCTGGAAAG-CGAAGAA-ATGCCCTATGGGCTTCGCAT	8253
Query	8257	ATGATACCCGCTGTTTTGACTCCACAGTCACTGAGAGCGACATCCGTACGGAGGAGGCAA	8316
Sbjct	8254	ATGACACCCGCTGTTTTGACTCAACGGTCACTGAGAATGACATCCGTGTTGAGGAGTCAA	8313
Query	8317	TTTACCAATGTTGTGACCTGGACCCCC-AAGCCCG-CGTGGCCATCAAG-TCCCTCACTG	8373
Sbjct	8314	TCTACCAATGTTGTGACTTGG-CCCCGAAGCCAGACA-GGCCAT-AAGGTCGCTCACAG	8370
Query	8374	AGAGGCTTTATGTTGGGGGGCCCTCTTACCAATTG-AAGGGGGGAAAACtGCGGCTACCGC	8432
Sbjct	8371	AGCGGCTTTACATCGGGGGCCCCCTGACTAATTCTAAAGGGC-AGAActGCGGCTATCGC	8429
Query	8433	AGGTGCCGCGCGAGCGGCGTACTGACAACtAGCTGTGGTAACACCCtCACTTGCTACATC	8492
Sbjct	8430	CGGTGCCGCGCGAGCGGTGTACTGACGACCAGCTGCGGTAATACCCtCACATGTTACTTG	8489
Query	8493	AAGGCC-CGGGCAGCCTGTCTGAGCCGC-AGGGCTCAGGACTGCACCATGCTCGTGTGTG	8550
Sbjct	8490	AAGGCCGCTG-CGGCCTGTCTGAGCTGCGAAG-CTCCAGGACTGCACGATGCTCGTATGCG	8547
Query	8551	GCGACGAC-TTAGTCGTTATCTGTGAAAGTGCGGGGGTCCAGGAGGACGCGGCGAGCCTG	8609
Sbjct	8548	GAGACGACCTT-GTCGTTATCTGTGAAAGCGCGGGGACCCAAAGAGGACGAGGCGAGCCT-	8605
Query	8610	A-GAGCCTTCACGGAGGCTATGACCAGGTACTCCGccccccccgggggagccc-cccACAAC	8667
Sbjct	8606	ACGGGCCTTCACGGAGGCTATGACTAGATACTCTGCCCCCCTGGGGACCCGCCCA-AAC	8664
Query	8668	CAGAATACGACTTGGAGCTT-ATAACATCATGCTCCTCCAACGTGTcAGTCGCCCACGAC	8726
Sbjct	8665	CAGAATACGACTTGGAG-TTGATAACATCATGCTCCTCCAATGTGTcAGTCGCGCACGAT	8723
Query	8727	GGCG-CTGG-AAAGAGGGTCTACTACCTTACCCGTGACCTTACAACCCCCCTCGCGAGAG	8784
Sbjct	8724	G-CATCTGGCAAA-AGGGTGTACTATCTCACCCGTGACCCACCACCCCCCTTGCGCGGG	8781
Query	8785	CCGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCTGGCTAGGCAACATAATCATGT	8844
Sbjct	8782	CTGCGTGGGAGACAGCTAGACACACTCCAGTCAATTCTGGCTAGGCAACATCATCATGT	8841
Query	8845	TTGCCCCACACT-GTGGGCGAGGATGATACTGATGACCCATTTCTT-TAGCGTCTT-CA	8901
Sbjct	8842	ATGCGCCAC-CTTGTTGGGCAAGGATGATCCTGATGACTCATTTCTTCTC-CATCCTTC-	8898
Query	8902	TAGC-CAGGGATCAGCTTGAACAGGCTCTTA-ACTGTGAGATCTACGGAGCCTGCTACTC	8959
Sbjct	8899	TAGCTCAGGAA-CAACTTGA AAAAGCCCT-AGATTGTcAGATCTACGGGGCCTGTTACTC	8956

Score = 3354 bits (1816), Expect = 0.0			
Identities = 3942/4944 (79%), Gaps = 244/4944 (4%)			
Strand=Plus/Plus			
Query	1	GCCAGCCCCCTGA-TGGGGGCGACACTCCACCATGA-ATCACTCCCCTGTGAGGAACACTAC	58
Sbjct	1	GCCAGCCCCC-GATTGGGGGCGACACTCCACCAT-AGATCACTCCCCTGTGAGGAACACTAC	58
Query	59	TGTCTTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTCAGCCTCCAGG	118
Sbjct	59	TGTCTTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTCAGCCTCCAGG	118
Query	119	AAAAAAAACTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCC	178
Sbjct	119	ACCCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCC	178
Query	179	AGGACGACCGGGTCTTTCTTGGATAAACCCGCTCAATGCCTGGAGATTGGGGCGTGCCC	238
Sbjct	179	AGGACGACCGGGTCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTGGGGCGTGCCC	238
Query	239	CCGCAAGACTGCTAGCCGAGTAGTGTGGGTCGCGAAAGGCCCTGTGGTACTGCCTGATA	298
Sbjct	239	CCGCGAGACTGCTAGCCGAGTAGTGTGGGTCGCGAAAGGCCCTGTGGTACTGCCTGATA	298
Query	299	GGGTGCTTGCAGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAA	358
Sbjct	299	GGGTGCTTGCAGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAA	358
Query	359	ACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCCACAGGACGTCAAGTTCCCGGG	418
Sbjct	359	ACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGGACGTCAAGTTCCCGGG	418

Query	419	TGGCGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGGCCCTAGATTGGGTGT	478
Sbjct	419	CGGTGGTCAGATCGTCGGTGGAGTTTACCTGTTGCCGCGCAGGGGCCCCAGGTGGGTGT	478
Query	479	GCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCC	538
Sbjct	479	GCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGGCGACAACCTATCCC	538
Query	539	CAAGGCACGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCCCCTCTA	598
Sbjct	539	CAAGGCTCGCCAGCCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACCCCTGGCCCCCTCTA	598
Query	599	TGGCAATGAGGG-TTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGGCCCTA	657
Sbjct	599	TGGCAATGAGGGCTTG-GGGTGGGCAGGATGGCTCCTGTACCCCGTGGCTCTCGGCCCTA	657
Query	658	GCTGGGGCCCCACAGACCCCCGGCGTAGGTTCGCGCAATTTGGGTAAGGTCATCGATACCC	717
Sbjct	658	GTTGGGGCCCCACGGACCCCCGGCGTAGGTTCGCGCAATTTGGGTAAGGTCATCGATACCC	717
Query	718	TTACGTGCGGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCCCTCTTGGAG	777
Sbjct	718	TCACGTGCGGGCTTCGCCGATCTCATGGGGTACATTCCGCTCGTCGGCGCCCCCTAGGGG	777
Query	778	GCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACATGCAA	837
Sbjct	778	GCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAACATGCAA	837
Query	838	CAGGGAACCTTCCTGGTTGCTC-TTCTCTATCTTCTTCTGGCCCTGCTCTCTTGCCTG	896
Sbjct	838	CAGGGAATCTGCCCGGTTGCTCCTTT-TCTATCTTCTTTTGGCTTTGCTGTCTGTTTG	896
Query	897	ACTGTGCCC-GCTTCAGCCTACCAAGTGCGCAAT-TCCTCGGG-GCTTTACCATGTCACC	953
Sbjct	897	ACCAT-CCCAGCTTCCGCTTATGAAGTGCGCAACGTA-TCCGGAG-TGTACCATGTCACG	953
Query	954	AATGATTGC-CCTAACTCGAGTATTGTGTACGAGGCGGCCGA--TGCCATCCTGCACACT	1010
Sbjct	954	AACGACTGCTCC-AACGCAAGCATTGTGTATGAGGCAGCGGACATG--ATCATGCATACC	1010
Query	1011	CCGGGGTGTTGT-CCCTTGCCTTCGCGAGGGTAACGCCTCGAGGTGTTGGGTGGCGGTGAC	1069
Sbjct	1011	CCCGGGTGCGTGCCCT-GCGTTCGGGAGAACAACTCCTCCCGCTGCTGGGTAGCGCTCAC	1069
Query	1070	CCCCACGGTGGCCACCAGGGACGGCAAAC-TCCCCACAACG-CAGCTTCGACGTCATATC	1127
Sbjct	1070	TCCCACGCTCGCGGGCCAGGAACG-CTAGCGTCCCCACTACGAC-GATACGACGCCATGTC	1127
Query	1128	GATCTGCTTGTTCGGGAGCGCCACC-CTCTGCTCGGCCCTCTACGTGGGGGACCTGTGCGG	1186
Sbjct	1128	GATTTGCTCGTTGGG-GCGGCTGCTCTCTGCTCCGCTATGTACGTGGGAGATCTCTGCGG	1186
Query	1187	GTCTGTCTTTCTT-GTTGGTCAACTGTTTACCTTCTCTCC-CAGGCGCCACTG-GACGAC	1243
Sbjct	1187	ATCTGT-TTTCCTCGTCGCCCAGCTGTTACCTTCTCGCCTC-GCCGGCAC-GAGAC-A-	1241
Query	1244	GCA-AG-ACTGCAATTGTTCTATCTATCCCGGCCATATAACGGGTATCGCATGGCATGG	1301
Sbjct	1242	GTACAGGACTGCAATTGCTCAATATATCCCGGCCACGTGACAGGTCACCGTATGGCTTGG	1301
Query	1302	GATATGATGATGAACCTGGTCCCCCTACGGCAGCGTTGGTGGTAGCTCAGCTGCTCCGGATC	1361
Sbjct	1302	GATATGATGATGAACCTGGTCACCTACAGCAGCCCTAGTGGTATCGCAGTTACTCCGGATC	1361
Query	1362	CCACAAGCCATCATGGACATGATCGCTGGTGCTCACTGGGGAGTCTGGCGGGCATAGCG	1421
Sbjct	1362	CCACAAGCTGTCTGGATATGGTGGCGGGGGCCCATGGGGAGTCTAGCGGGCCTTGCC	1421
Query	1422	TATT-TCTCCATGGTGGGGAACTGGGCGAAGGTCCTGGTAGTGTGCTGCTATTTGCCGG	1480
Sbjct	1422	TACTAT-TCCATGGTGGGGAACTGGGCTAAGGTTCTGATTGTGATGCTACTCTTTGCCGG	1480
Query	1481	CGTCGACGCGGAAACCCACGTCACCGGGGGAAATGCCGGCCGCAC-CACGGCT-GGGCTT	1538
Sbjct	1481	CGTTGACGGGGGAACCTATGTGACAGGGGGGAC-GATGGCCAAAAACACC-CTCGGGATT	1538

Query	1539	--GTTGGTCTCCTTACACCAGGCGCCAAGC--AGAACATCCAACCT--GATCAACACCAACGG	1594
Sbjct	1539	ACGTCCCTCTT--TT--CACCCGG--GTCATCCCAGAAAATCCAGCTTG--TAAACACCAACGG	1594
Query	1595	CAGTTGGCACATCAATAGCACGGCCTTGAATTGCAATGAAAGCCTTAACACCGGCTGG--T	1653
Sbjct	1595	CAGCTGGCACATCAACAGGACTGCCCTGAACTGCAATGACTCCCTCAACACTGGGTTTCCT	1654
Query	1654	TAGCAGGGCTCTTCTATCAA--CACAAATTCAACTCTTCAGGCTGTCCTGAGAGGTTGGCC	1712
Sbjct	1655	T--GCTGCGCTGTTCTA--CGTGCACAAGTTCAACTCATCTGGATGCCAGAGCGCATGGCC	1712
Query	1713	AGCTGCCGACGCCTT--AC--CGATTTTGGCCAGGGCTGGGGTCTTATCAGTTATGCCAAC	1769
Sbjct	1713	AGCTGCAGCC--CCATCGACGCG--TTC--GCTCAGGGGTGGGGGCCCATCACTTA--C--AAT	1766
Query	1770	G--G--A--AGCGGCCTCG--ACGA--ACGCCCCTACTGCTGGCACTACCTTCCAAGACCTTGT	1823
Sbjct	1767	GAGTCACA--CAGC--TCGGACCAGAGGCCT--TATTGTTGGCACTACGCACCCCGGCCGTGC	1823
Query	1824	GGCATTGTGCCCCGAAAG--AGCGTGTGTGGCCCGGTATATTGCTTCACTCCCA--GCCCCG	1881
Sbjct	1824	GGTATCGTACCCGCGGCGCAG--GTGTGTGGTCCAGTGTACTGCTTCAC--CCCAAGCCCTG	1881
Query	1882	TGGTGGTGGGAACGACCGACAGGT--CGGGCG--CGCCTACCTACAGCTGGGGTGCA--AATG	1938
Sbjct	1882	TCGTGGTGGGGACGACCGACCGGTTTCGG--CGTC--CCTACGTACAGTTGGGGGG--AGAATG	1938
Query	1939	ATACGGATGT--CTTCGTCCTTAACAACAC--CAGGCCACCGCTGGGCAATTGGTTCGGTTG	1996
Sbjct	1939	AGACGGACGTGCTGCTTC--TTAACAACACGC--GGCCGCCGCAAGGCAACTGGTTTGGCTG	1996
Query	1997	TACCTGGATGAACT--CAACTGGATTACCAA--AGTGTGCGGAGCGCCCCCTTGTGT--C	2051
Sbjct	1997	TACATGGATGAA--TAGCA--CTGGGTTACCAAGAC--GTGCGGGG--GCCCCC--GTGTAAC	2051
Query	2052	ATCGGAGGGG--TGGGCAACAACACCTTG--CTCTGCCCCACTGATTGCTTCCGCAAACATC	2109
Sbjct	2052	ATCGG--GGGGATCGGCAATAAAACCTTGAC--CTGCCCCACGGACTGCTTCCGGAAGCACC	2109
Query	2110	CGGAAGCCACATACTCTCG--GTGCGGCTCCGGTCCCTGGATT--ACACCCAGGTGCATGGT	2167
Sbjct	2110	CCGAGGCCACTTACAC--CAAGTGTGGTTCGGGGCCTTGG--TTGACACCCAGATGCTTGGT	2167
Query	2168	CGACTACCCGTATAGGCTTTGGCACTATCCTTGTACCATCAA--TTACACCATATTCAAAG	2226
Sbjct	2168	CCACTACCCATACAGGCTTTGGCACTACCCCTGCACTGTCAACTTT--ACCATCTTCAAGG	2226
Query	2227	TCAGGATGTACGTGGGAGGG--GTCGAGCACAGGCTGGAAGCGGCCTGCAACTGGACGCGG	2285
Sbjct	2227	TTAGGATGTACGTGGG--GGGAGTGGAGCACAGGCTCGAAGCCGCATGCAATTGGACTCGA	2285
Query	2286	GGCGAACGCTGTGATCTGGAAGACAGGGACAGGTCCGAGCTCAGCCCGTTGCTGCTGTCC	2345
Sbjct	2286	GGAGAGCGTTGTAACCTGGAGGACAGGGACAGATCAGAGCTTAGCCCGCTGCTGCTGTCT	2345
Query	2346	ACCACACAGTGGCAGGTCCTT--CCGTGTTCTTTACGACCCTGCCAGC--CTTGTCCACCG	2403
Sbjct	2346	ACAACGGAGTGGCAGGTA--TTGCCCTGTTCTTACCACCCTACCGGCTCT--GTCCACTG	2403
Query	2404	GCCTCATCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGGTAGGGTCAA	2463
Sbjct	2404	GTTTGATCCATCTCCATCAGAACGTCGTGGACGTACAATACCTGTACGGTATAGGGTCG--	2462
Query	2464	GCA--TCG--CGTCCTGGGCCATTAAAGTGGGAGTACGTCGT--TCTCCTGTTCTTCTGCTTG	2520
Sbjct	2463	GCGGTTGTC--TCCTTTGCAATCAAATGGGAGTATGTCCTGT--TGCTCTTCCTTCTTCTGG	2520
Query	2521	CAGACGCGCGCGTCTGCT--CCTGCTTGTGGATGATGTTACTCATATCCCAAGCGGAGGCG	2579
Sbjct	2521	CGGACGCGCGCGTCTG--TGCTGCTTGTGGATGATGCTGCTGATAGCTCAAGCTGAGGCC	2579
Query	2580	GCTTTGGAGAACCTCGTAATACTCAATGCAGCATCCCTGGCCGGGACGCACGGTC--TTGT	2638
Sbjct	2580	GCCCTAGAGAACCTGGTGGTCTCAACGCGGCATCCGTGGCCGGGGCGCATGG--CATTCT	2638

Query	2639	GTCCTTCCTCGTGTTCCTTCTGCTT-TGCGTGGTATC-TGAAGGGTAGG-TGGGTGCCC-G	2694
Sbjct	2639	CTCCTTCCTCGTGTTCCTTCTG-TGCTGCCTGGTA-CATCAAGGGCAGGCTGG-T-CCCTG	2694
Query	2695	GAGCGGTC-TACGCCCTCTACGG-GATGTGGCCTCTCCTCCTGCTCCTGCTGGCGTTGCC	2752
Sbjct	2695	GGGCGG-CATATGCCCTCTACGGCG-TATGGCCGCTACTCCTGCTCCTGCTGGCGTTACC	2752
Query	2753	TC-AGCGGGCATAACGC-ACTGGACACGG-AGGTGGCCGCGTCGTGTGGCGGCGTTGTTCT	2809
Sbjct	2753	ACCA-CGAGCATAACGCCA-TGGAC-CGGGAGATGGCAGCATCGTGCAGGAGCGCGGTT-T	2808
Query	2810	T-GTCGGGT-TAATGGCGCT-GACTCT-GTCGCCATATTACAAGC-GCTATATCAGCT-G	2863
Sbjct	2809	TCGTAGG-TCTGATA-CTCTTGAC-CTTGTCAACGCACTATAAGCTGTTCC-TC-GCTAG	2863
Query	2864	G-TGCAATGTGGTGGCTT-CAGTATTTTCTGACCAGAGTAGAAGCGCAACT-GCACGTGTG	2920
Sbjct	2864	GCT-CATATGGTGG-TTACAATATTTTATCACCAGGGCCGAGGCACA-CTTGCAAGTGTG	2920
Query	2921	GGTTTCAACGTCCCGCGATGCCGTCATCTTACTCATGTGTGT-AG	2979
Sbjct	2921	GATCCCCCCCCCTCAACGTTTCGGGGGGGCCGCGATGCCGTCATCTCCTCACGTGCGCGA-	2979
Query	2980	TACACCC-GACCCTGGTATTTGAC-ATCACCAAACCTACTC-CTGGCCAT-CTTCGGACCC	3035
Sbjct	2980	TCCACCCAGAGC-TAATCTTT-ACCATCACCAAAT-CTTGCTCGCCATACT-CGGTCCA	3035
Query	3036	CTT-TGGATTCTTCAAGCCAGTTTG-CTTAAAGTCCCTACTTCGTGCGCGTTCAAGGCC	3093
Sbjct	3036	CTCATGG-TGCTCCAGGCTGGTATAACC-AAAGTGCCGTACTTCGTGCGCGCACACGGGC	3093
Query	3094	TTC-TCCG-G-ATCTGCGCGCTAGCGCGGAAGATAGCCGGAGGTCATTACGTGCAAATGG	3150
Sbjct	3094	T-CATTCTGTGCAT--GCATGCTGGTGCAGGAAGGTTGCTGGGGGTCATTATGTCCAAATGG	3150
Query	3151	C-CATCATCAAGTTAGGG-GCGCTTACTGGCACCTATGTGTATAACCATCTCACCCCTCT	3208
Sbjct	3151	CTC-TCATGAAGTT-GGCCGCACTGACAGGTACGTACGTTTATGACCATCTCACCCCACT	3208
Query	3209	TCGAGACTGGGCGCACAAACGG-CCTGCGAGATCTGGCCGTGGCTGTGGAACCAAGTCGTCT	3267
Sbjct	3209	GCGGGACTGGGCCCACG-CGGGCCCTACGAGACCTTGCGGTGGCAGTTGAGCCCGTCGTCT	3267
Query	3268	TCTCCCGA-ATGGAGACCAAGCTCATCACGTGGGGGGCAGATACCGCCGCGTGCAGTGAC	3326
Sbjct	3268	TCTCT-GATATGGAGACCAAGGTTATCACCTGGGGGGCAGACACCGCGGCGTGTGGGGAC	3326
Query	3327	ATCATCAACGGCTTGCCCCGTCTCTGCCCCGTAGGGGCCAGG-AGATAC-TGCTTGGG-CCA	3383
Sbjct	3327	ATCATCTTGGGCCTGCCCCGTCTCCGCCCCGAGGGGG-AGGGAGATACAT-CT-GGGACCG	3383
Query	3384	GCCGACGGAATGGTCTC-CAAGGGGTGGAGGTTGCTGGCGCCCATCACGGCGTACGCCCA	3442
Sbjct	3384	GCAGACAGCCTTGAAGGGCA-GGGGTGGCGACTCCTCGCGCCTATTACGGCCTACTCCCA	3442
Query	3443	GCAGACGAGAGGCCCTCCTAGGGTGTATAATCACCAGCCTGACTGGCCGGGACAAAACCA	3502
Sbjct	3443	ACAGACGCGAGGCCCTACTTGGCTGCATCATCACTAGCCTCACAGGCCGGGACAGGAACCA	3502
Query	3503	AGTGGAGGGTGAGGTCCA-GATCGTGTCAACTGCTACCCAAACCTTCTGGCAACGTGCA	3561
Sbjct	3503	GGTCGAGGGGGAGGTCCAAG-TGGTCTCCACCGCAACACAATCTTTCTGGCGACCTGCG	3561
Query	3562	TCAATGGGGTATGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCGCATCACCCA	3621
Sbjct	3562	TCAATGGCGTGTGTTGGACTGTCTATCATGGTGCCGGCTCAAAGACCCTTGCCGG-CCCA	3620
Query	3622	A-GGGTCCTGTTCATCCAGATGTATAACCAATGTGGACCAAGACCTTGTGGGCTGGCCCGCT	3680
Sbjct	3621	AAGGGCCCAATCACCCAAATGTACACCAATGTGGACCAGGACCTCGTCGGCTGGCAAGCG	3680
Query	3681	CCTCAAGGTTCCCGCTCATTTGACACCCTGTACCTGCGGCTCCTCGGACCTTTACCTGGTC	3740
Sbjct	3681	CCCCCGGGGCGCGTTCTTTGACACCATGCACCTGCGGCAGCTCGGACCTTTACTTGGTC	3740

Query	3741	ACGAGGCACGCCGATGTCATTCCCCTGCGCCGGCGAGGTGATAGCAGGGGTAGCCTGCTT	3800
Sbjct	3741	ACGAGGCATGCCGATGTCATTCCGGTGCGCCGGCGGGGCGACAGCAGGGGGAGCCTACTC	3800
Query	3801	TCGCCCC-GGCCCATTTCCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCCGC	3859
Sbjct	3801	TC-CCCCAGGCCCCGTCTCCTACTTGAAGGGCTCTTCGGGCGGTCCACTGCTCTGCCCTC	3859
Query	3860	GGGACACGCCGTGGGCCTATT-CAGGGCCGCGGTGTGCACCCGTGGAGTGGCTAAAGCGG	3918
Sbjct	3860	GGGGCACGCTGTGGGCATCTTTC-GGGCTGCCGTGTGCACCCGAGGGGTTCGCAAGGCGG	3918
Query	3919	TGGACTTTAT-CCCTGTGGAGAACCTAGGGACAACCA-T--GAGATCCCCGGTGTTCACG	3974
Sbjct	3919	TGGACTTTGTACCC-GTCGAGT-C-TATGGA-AACCACTATGCGGTCCCCGGTCTTCACG	3974
Query	3975	GACAACTCCTCTCCACCAGCAGTGCCCCAGAGC-TTCCAGGTGGCCACCTGCATGCTCC	4033
Sbjct	3975	GACAACTCGTCCCTCCGGCCGTACCGCAGA-CATTCCAGGTGGCCCATCTACACGC-CC	4032
Query	4034	C-ACCGGCAGCGGTAAGAGCACCAAGTCCCGGCTGCGTACGCAGCCCA-GGGCTACAAG	4091
Sbjct	4033	CTACTGGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCGTATGCAGCCCAAGGG-TATAAG	4091
Query	4092	GTG-TTGGTGCTCAACCCCTCTGTTGCTGCAACGCTGGGCTTT-GGTGCTTACATGTCCA	4149
Sbjct	4092	GTGCTTG-TCCTGAACCCGTCCGTGCGCCGCCACCCTAGG-TTTCGGGGCGTATATGTCTA	4149
Query	4150	AGGCCCATGGGGTTGATCCTAATATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCC	4209
Sbjct	4150	AGGCACATGGTATCGACCCTAACATCAGAACCAGGGGTAAAGGACCATCACACGGGT-GCC	4208
Query	4210	CC-ATCACGTACTCCACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCAGGAGGTGCT	4268
Sbjct	4209	CCCATCACGTACTCCACCTATGGCAAGTTTCTTGCCGACGGTGGTTGCTCTGGGGGCGCC	4268
Query	4269	TATGACATAATAATTTGTGACGAGTGCCACTCCACGGA-T-G-CCACATCCATCTTGGGC	4325
Sbjct	4269	TATGACATCATAATATGTGATGAGTGCCACTCAACTGACTCGACCAC-T--ATCCTGGGC	4325
Query	4326	ATCGGCACGTGTCCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACT	4385
Sbjct	4326	ATCGGCACAGTCTTGACCAAGCGGAGACGGCTGGAGCGCGACTCGTCGTGCTCGCCACC	4385
Query	4386	GCTACCCCTCCGGGCTCCGTCACTGTGTCC-CATCCTAACATCGAGGAGGTTGCTCTGTC	4444
Sbjct	4386	GCTACGCCCTCCGGGATCGGTCACCGTG-CCACATCCAAACATCGAGGAGGTGGCTCTGTC	4444
Query	4445	CACCACCGGAGAGATCCCCCTTTTACGGCAAGGCTATCCCCCTCGAGGTGATCAAGGGGGG	4504
Sbjct	4445	CAGCACTGGAGAAATCCCCCTTTTATGGCAAAGCCATCCCCATCGAGACCATCAAGGGGGG	4504
Query	4505	AAGACATCTCATCTTCTGCCACTCAAAGAAGAAGTGCGACGAGCTCGCCGCGAAGCTGGT	4564
Sbjct	4505	GAGGCACCTCATTTTCTGCCATTCCAAGAAGAAATGTGATGAGCTCGCCGCGAAGCTG-T	4563
Query	4565	C-G-CATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCTGTATCCCCG	4622
Sbjct	4564	CCGGCCTCGGAC-TCAATGCTGTAGCATATTACCGGGGCCCTTGATGTATCCGTCATACCA	4622
Query	4623	ACCAGCGGCGATGTTGTCTGCTGT-GTCGACCGATGCTCTCATGACTGGCTTTACCGGCGA	4681
Sbjct	4623	ACTAGCGGAGACGTCATTGTCTGTAG-CAACGGACGCTCTAATGACGGGCTTTACCGGCGA	4681
Query	4682	CTTCGACTCTGTGATAGACTGCAACACGTGTGTCACTCAGACAGTCGATTTTACGCTTGA	4741
Sbjct	4682	TTTCGACTCAGTGATCGACTGCAATACATGTGTACCCAGACAGTCGACTTCAGCTTGA	4741
Query	4742	CCCTACCTTTTACCATTGAGACAACCAC-GCTCCCCCAGGATGCTGTCTCCAGGACTCA-A	4799
Sbjct	4742	CCCGACCTTCACCATTGAGACGACGACCG-TGCCACAAGACGCGGTGTC-ACG-CTCGCA	4798
Query	4800	-CGCCGGGGCAGGACTGGCAGGGG	4822
Sbjct	4799	GCGGCGAGGCAGGACTGGTAGGGG	4822

[Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)